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5'	GGC	TTC	TGG	GAG	CNA	CCG	CTC	CGC	TGC	TCT	CGT	TGG	TTC	CGG	AGG	TCG	CTG	CGG
	63					72			81			90			99			108
	CGG	TGG	GAA	ATG	CTG	GCG	CGC	GCG	GCG	CGG	GGG	CAC	TGG	GGC	CCT	TTT	GCT	GAG
			M	L		A	R	A	A	R	G	H	W	G	P	F	A	E
	117					126			135			144			153			162
	GGG	CTC	TCT	ACT	GGC	TTC	TGG	CCG	CGC	TCC	GGC	CGC	GCC	TCC	TCT	GGA	TTG	CCC
	G	L	S	T	G	F	W	P	R	S	G	R	A	S	S	G	L	P
	171					180			189			198			207			216
	CGA	AAC	ACC	GTG	GTA	CTG	TTC	GTG	CCG	CAG	CAG	GAG	GCC	TGG	GTG	GTG	GAG	CGA
	R	N	T	V	V	L	F	V	P	Q	Q	E	A	W	V	V	E	R
	225					234			243			252			261			270
	ATG	GGC	CGA	TTC	CAC	CGG	ATC	CTG	GAG	CCT	GGT	TTG	AAC	ATC	CTC	ATC	CCT	GTG
	M	G	R	F	H	R	I	L	E	P	G	L	N	I	L	I	P	V
	279					288			297			306			315			324
	TTA	GAC	CGG	ATC	CGA	TAT	GTG	CAG	AGT	CTC	AAG	GAA	ATT	GTC	ATC	AAC	GTG	CCT
	L	D	R	I	R	Y	V	Q	S	L	K	E	I	V	I	N	V	P
	333					342			351			360			369			378
	GAG	CAG	TCG	GCT	GTG	ACT	CTC	GAC	AAT	GTA	ACT	CTG	CAA	ATC	GAT	GGA	GTC	CTT
	E	Q	S	A	V	T	L	D	N	V	T	L	Q	I	D	G	V	L
	387					396			405			414			423			432
	TAC	CTG	CGC	ATC	ATG	GAC	CCT	TAC	AAG	GCA	AGC	TAC	GGT	GTG	GAG	GAC	CCT	GAG
	Y	L	R	I	M	D	P	Y	K	A	S	Y	G	V	E	D	P	E
	441					450			459			468			477			486
	TAT	GCC	GTC	ACC	CAG	CTA	GCT	CAA	ACA	ACC	ATG	AGA	TCA	GAG	CTC	GGC	AAA	CTC
	Y	A	V	T	Q	L	A	Q	T	T	M	R	S	E	L	G	K	L
	495					504			513			522			531			540
	TCT	NTG	GAC	AAA	GTC	TTC	CGG	GAA	CGG	GAG	TCC	CTG	AAT	GCC	AGC	ATT	GTG	GAT
	S	X	D	K	V	F	R	E	R	E	S	L	N	A	S	I	V	D
	549					558			567			576			585			594
	GCC	ATC	AAC	CAA	GCT	GCT	GAC	TGC	TGG	GGT	ATC	CGC	TGC	CTN	CGT	TAT	GAG	ATC
	A	I	N	Q	A	A	D	C	W	G	I	R	C	L	R	Y	E	I
	603					612			621			630			639			648
	AAG	GAT	ATC	CAT	GTG	CCA	CCC	CGG	GTG	AAA	GAG	TCT	ATG	CAG	ATG	CAG	GTG	GAG
	K	D	I	H	V	P	P	R	V	K	E	S	M	Q	M	Q	V	E
	657					666			675			684			693			702
	GCA	GAG	CGG	CGG	AAA	CGG	GCC	ACA	GTT	CTA	GAG	TCT	GAG	GGG	ACC	CGA	GAG	TCG
	A	E	R	R	K	R	A	T	V	L	E	S	E	G	T	R	E	S

FIGURE 1A

711 720 729 738 747 756  
 GCC ATC AAT GTG GCA GAA GGG AAG AAA CAG GCC CAG ATC CTG GCC TCC GAA GCA  
 A I N V A E G K K Q A Q I L A S E A  
 765 774 783 792 801 810  
 GAA AAG GCT GAA CAG ATA AAT CAG GCA GCA GGA GAG GCC AGT GCA GTT CTG GCG  
 E K A E Q I N Q A A G E A S A V L A  
 819 828 837 846 855 864  
 AAG GCC AAG GCT AAA GCT GAA GCT ATT CGA ATC CTG GCT GCA GCT CTG ACA CAA  
 K A K A K A E A I R I L A A A L T Q  
 873 882 891 900 909 918  
 CAT AAT GGA GAT GCA GCA GCT TCA CTG ACT GTG GCC GAG CAG TAT GTC AGC GCG  
 H N G D A A A S L T V A E Q Y V S A  
 927 936 945 954 963 972  
 TTC TCC AAA CTG GCC AAG GAC TCC AAC ACT ATC CTA CTG CCC TCC AAC CCT GGC  
 F S K L A K D S N T I L L P S N P G  
 981 990 999 1008 1017 1026  
 GAT GTC ACC AGC ATG GTG GCT CAG GCC ATG GGT GTA TAT GGA GCC CTC ACC AAA  
 D V T S M V A Q A M G V Y G A L T K  
 1035 1044 1053 1062 1071 1080  
 GCC CCA GTG CCA GGG ACT CCA GAC TCA CTC TCC AGT GGG AGC AGC AGA GAT GTC  
 A P V P G T P D S L S S G S S R D V  
 1089 1098 1107 1116 1125 1134  
 CAG GGT ACA GAT GCA AGT NTT GAT GAG GAA CTT GAT CGA GTC AAG ATG AGT TAG  
 Q G T D A S X D E E L D R V K M S \*  
 1143 1152 1161 1170 1179 1188  
 TGG AGC TGG GCT TNG CCA GGG AGT CTG GGG ACA AGG AAG CAG ATT TTC CTG ATT

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FIGURE 1B



148	R	-	-	E	R	E	S	L	N	A	S	I	V	D	A	I	N	A	A	D	C	W	G	I	R	C	L	R	Y	E	I	K	D	I	H	V	P	P	R	789094	
165	S	-	-	D	R	E	I	A	H	N	M	Q	S	T	L	D	D	A	T	D	A	W	G	I	K	V	E	R	V	E	I	K	D	V	K	L	P	V	Q	GI 31069	
170	S	-	-	D	R	E	T	L	A	S	M	Q	T	I	L	D	E	A	T	E	S	W	G	I	K	V	E	R	V	E	I	K	D	V	R	L	P	I	Q	GI 1065452	
197	S	S	Q	D	R	R	I	I	S	A	N	L	K	D	E	L	G	S	F	T	C	Q	F	G	V	E	I	T	D	V	E	I	S	D	V	K	I	-	GI 1353669		
136	T	-	-	S	R	D	Q	I	N	A	Q	L	R	G	V	L	D	E	A	T	G	R	W	G	L	R	V	A	R	V	E	L	R	S	I	D	P	P	S	779701	
134	N	-	-	K	R	E	Y	I	N	S	K	L	L	E	I	L	D	R	E	T	D	A	W	G	V	R	I	E	K	V	E	V	K	E	I	D	P	P	E	GI 1591514	
186	V	K	E	S	M	O	M	Q	V	E	A	E	R	R	K	R	A	T	V	L	E	S	E	G	T	R	E	S	A	I	N	V	A	E	G	K	K	Q	A	Q	789094
203	L	Q	R	A	M	A	E	A	E	A	S	R	R	E	A	R	A	K	V	I	A	A	E	G	E	M	N	A	-	-	-	-	-	-	-	-	-	-	GI 31069		
208	L	Q	R	A	M	A	E	A	E	A	T	R	E	A	R	A	K	V	I	A	A	E	G	E	Q	K	A	-	-	-	-	-	-	-	-	-	-	GI 1065452			
234	V	K	E	G	E	N	M	G	M	S	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1353669					
174	I	Q	A	S	M	E	K	Q	M	K	A	D	R	E	K	R	A	M	I	L	T	A	E	G	T	R	E	A	I	K	Q	A	E	G	Q	K	Q	A	Q	779701	
172	I	K	N	A	M	A	Q	Q	M	K	A	E	R	L	K	R	A	A	I	L	E	A	E	G	E	K	P	E	-	-	-	-	-	-	-	-	-	GI 1591514			
226	I	L	A	S	E	A	E	K	A	E	Q	I	N	O	A	G	E	A	S	A	V	L	A	K	A	K	A	E	A	I	-	-	-	-	-	-	-	-	789094		
231	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 31069					
236	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1065452					
260	V	I	G	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1353669				
214	I	L	A	E	G	A	K	Q	A	A	I	L	A	E	A	D	R	Q	S	R	M	L	R	A	Q	G	E	R	A	A	A	Y	L	Q	A	Q	Q	Q	779701		
259	-	R	I	L	A	A	A	L	T	O	H	N	G	D	A	A	A	S	L	T	V	A	E	Q	Y	V	S	A	F	S	K	L	A	K	D	S	N	T	I	L	789094
244	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 31069				
249	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1065452				
288	S	D	V	P	S	T	S	A	A	G	T	S	T	D	T	P	N	I	P	S	I	D	I	D	H	L	I	S	V	A	S	L	A	M	D	E	H	-	L	V	GI 1353669
254	A	K	A	I	E	K	T	F	A	A	I	K	A	G	R	P	T	P	E	M	L	A	Y	Q	L	Q	T	L	P	E	M	A	R	G	D	A	N	K	V	779701	
298	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	789094				
268	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 31069				
269	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1065452					
327	R	L	I	G	R	V	F	Q	I	N	C	K	D	I	E	P	-	I	C	I	D	L	K	H	G	S	G	S	A	Y	K	G	T	S	L	-	-	N	P	D	GI 1353669
294	W	V	V	P	S	D	F	N	A	A	L	Q	G	F	T	R	L	L	G	K	P	G	E	D	G	V	F	-	R	F	E	P	S	P	V	E	D	Q	P	K	779701

FIGURE 2B

330	S L S S G S S R D V O G	- - - - T D A S X D E E L D	- - - - R V K	- - - - 789094
276	- - - - -	- - - - -	- - - - -	- - - - L GI 31069
276	- - - - -	- - - - -	- - - - -	- - - - S GI 1065452
364	V V F E - T S L E V F G	K I L T K E V S P V T V Y M N G N L K	V K G S I Q D A M	GI 1353669
333	H A A D G D D A E V A G	T D P S I A R A V A - - -	T A E A I A R K P V	Z 79701

FIGURE 2C

Library	Lib Description	Abun	Pct	Abun
PROSTUT03	prostate tumor, 67 M, match to PROSNOT05	2	0.0703	
COLNNOT05	colon, 40 M, match to COLNCRT01	2	0.0577	
TESTNOT03	testis, 37 M	1	0.0557	
LIVRNOT02	liver, 32 F	1	0.0515	
HUVENOB01	HUVEC endothelial cell line, control	1	0.0418	
LVENNOT03	heart, left ventricle, 31 M	1	0.0336	
PROSTUT01	prostate tumor, 50 M, match to PROSNOT02	1	0.0309	
PANCTUT02	pancreatic tumor, carcinoma, 45 F	1	0.0288	
KERANOT01	keratinocytes, neonatal M	1	0.0227	
CRBLNOT01	brain, cerebellum, 69 M	1	0.0194	
LUNGNOT04	lung, 2 M	1	0.0182	
PGANNOT01	paraganglia, 46 M	1	0.0159	
BRSTTUT01	breast tumor, 55 F, match to BRSTNOT02	1	0.0150	

FIGURE 3